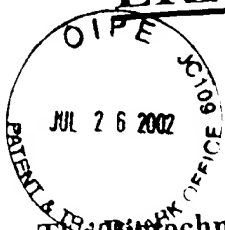
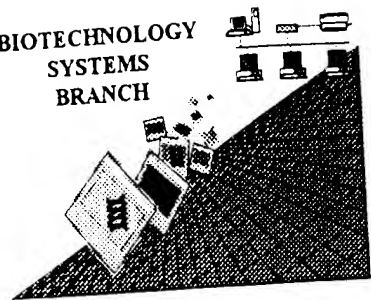


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/453,980
Art Unit / Team No.: BATCH 1615-3/17
Date Processed by STIC: 4/13/2000

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THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-508-4212

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/403,980

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length
Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 Skipped Sequences (OLD RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES)
Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES)
Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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PAGE: 1

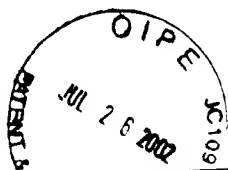
RAW SEQUENCE LISTING
PATENT APPLICATION US/09/403,980

BATCH

(1515)
(3-17)

DATE: 04/13/2000
TIME: 13:47:38

Input Set: I403980.RAW



This Raw Listing contains the General Information
Section and up to first 5 pages.

PR.54

1 <110> APPLICANT: I.N.S.E.R.M.
2 <120> TITLE OF INVENTION: NEW POLYPEPTIDES ASSOCIATED WITH ACTIVATORY RECEPTORS
3 AND THEIR BIOLOGICAL APPLICATIONS
4 <130> FILE REFERENCE: PCT/FR98/00883
5 <140> CURRENT APPLICATION NUMBER: US/09/403,980
6 <141> CURRENT FILING DATE: 2000-01-19
7 <150> EARLIER APPLICATION NUMBER: FR97/05411
8 <151> EARLIER FILING DATE: 1997-04-30
9 <160> NUMBER OF SEQ ID NOS: 31
10 <170> SOFTWARE: PatentIn Ver. 2.1
11 <210> SEQ ID NO 1
12 <211> LENGTH: 517
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17 ggggctctgg agcctcctgg tgccttctgt tcttctctgt cctcctgact gtgggaggat 120
18 taagtcccgat acaggcccag agtgacactt tcccaagatg cgactgttct tccgtgagcc 180
19 ctggtgtact gtctgggatt gttctgggtg acttgggtgt gactctgctg attgccctgg 240
20 ctgtgtactc tctggggccgc ctggtctccc gaggtcaagg gacagcggaa gggaccggga 300
21 aacaacacat tgetgagact gagtgccttt atcaggagct tcagggtcag agacatgaag 360
22 tatacagtga cctcaacaca cagaggcaat attacagatg agcccactct atgcccacat 420
23 gcgccctgat gcccgatcc ggtcattcca gatgcctact caacaagccc tctctgagat 480
24 caggactccc gttggaatac agatccacag ggtacct 517
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26 <211> LENGTH: 87
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33 20 25 30
34 Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly
35 35 40 45
36 Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro
37 50 55 60
38 Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn 80
39 65 70 75
40 Thr Gln Arg Gln Tyr Tyr Arg 85
41
42 <210> SEQ ID NO 3
43 <211> LENGTH: 16
44 <212> TYPE: PRT

Does Not Comply
Corrected Diskette Needed

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/403,980DATE: 04/13/2000
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Input Set: I403980.RAW

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46 <400> SEQUENCE: 3
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50 <211> LENGTH: 24
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52 <213> ORGANISM: Mus musculus
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57 20
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60 <212> TYPE: PRT
61 <213> ORGANISM: Mus musculus
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68 35 40
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75 ggctctggag cctcctgggtg ccttctgttc cttcctgtcc tcctgactgt gggaggatta 120
76 agtcccgtac aggccagag tgacactttc ccaagatgag actgttcttc cgtgagccct 180
77 ggtgtactgt ctgggattgt tctgggtgac ttgggtgtga ctctgctgat tgccctggct 240
78 gtgtactctc tgggcccgtt ggtctccga ggtcaaggga cagcggagg gaccggaaa 300
79 caacacattg ctgagactga gtcgccttat caggagcttc agggctcagag acatgaagta 360
80 tacagtgacc tcaacacaca gaggcaatat tacagatgag cccactctat gcccatcagc 420
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90 ggcactgttc ttccgtgagc cctgggtgtac tggctgggat tgttctgggt gacttgggtg 180
91 tgactctgct gattgccctg gctgtgtact ctctcgcccg cctgggtctcc cgagggtcaag 240
92 ggacagcgga agggaccgg aaacaacaca ttgctgagac tgagtgcct tatcaggagc 300
93 ttcagggtca gagaccagaa gtatacagt acctcaacac acagaggcaa tattacagat 360
94 gagccactc t 371

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Input Set: I403980.RAW

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96 <211> LENGTH: 376
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101 gtgacacttt cccaagatgc ggctgttctt ccgtgagccc tgggtgtactg gctgggattg 120
102 ttctgggtga cttggtgttg actctgctga ttgccctggc tgtgtactct ctgggccggc 180
103 tggctctccc aggtcaaggg acagcggaag ggacccggaa acaacacatt gctgagactg 240
104 agtcgcctta tcaggagctt cagggtcaga gacatgaagt atacagtgc ctcaacacac 300
105 agaggcaata ttacagatga gccactcta tgcccatcag cggcctgatg cccggatccg 360
106 gtcattccag atgcct 376
107 <210> SEQ ID NO 9
108 <211> LENGTH: 402
109 <212> TYPE: DNA
110 <213> ORGANISM: Mus musculus
111 <400> SEQUENCE: 9
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113 ctggtgcctt ctgttcttc ctgtcctcct gactgtggga ggattaagtc ccgtacaggc 120
114 ccagagtgc actttccaa gatgcgactg ttcttcctg agccctgggtg tactggctgg 180
115 gattgttctg ggtgacttgg tgttgactct gctgattgcc ctggctgtgt actctctggg 240
116 ccgctgggtc tcccaggtc aaggacagc ggaaggacc cggaaacaac acattgctga 300
117 gactgagtcg cttatcagg agcttcaggg tcagagacca gaagtataca gtgacctcaa 360
118 cacacagagg caatattaca gatgagccac tctatgccca tc 402
119 <210> SEQ ID NO 10
120 <211> LENGTH: 482
121 <212> TYPE: DNA
122 <213> ORGANISM: Mus musculus
123 <400> SEQUENCE: 10
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125 tttcccaaga tgcgactgtt cttccgtgag ccctgggtgta ctggctggga ttgttctggg 120
126 tgacttggtg ttgactctgc tgattgccct ggctgtgtac tctctgggcc gcttggtctc 180
127 ccgaggtcaa gggacagcgg aagggaaccg gaaacaacac attgctgaga ctgagtcgcc 240
128 ttatcaggag cttcagggtc agagacctga agtatacagt gacctcaaca cacagaggcg 300
129 atattacaga tgagcccact ctatgcccat cagcggcctg atgcccggat ccggtcattc 360
130 cagatgccta ctcaacaagc cttctgtgg gatcaggact ccggttgga tacagatcca 420
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136 <213> ORGANISM: Mus musculus
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139 1 5 10
140 Trp Pro Pro Trp Gly Ser Gly Ala Ser Trp Cys Leu Leu Phe Leu Pro 30
141 20 25
142 Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp 45
143 35 40
144 Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ser
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RAW SEQUENCE LISTING PATENT APPLICATION US/09/403,980

DATE: 04/13/2000
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Input Set: I403980.RAW

W--> 145 50 55 60
146 Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala 80
147 65 70 75
148 Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu 95
149 85 90
150 Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu 110
151 100 105 110
152 Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg 125
153 115 120 125
154 Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile Ser Gly Leu Met Pro 140
155 130 135
156 Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Ser Leu Arg Ser 160
157 145 150 155
158 Gly Leu Pro Leu Glu Tyr Arg Ser Thr Gly Tyr 170
159 165
160 <210> SEQ ID NO 12
161 <211> LENGTH: 123
162 <212> TYPE: PRT
163 <213> ORGANISM: Mus musculus
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166 1 5 10
167 Phe Leu Pro Val Leu Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala 30
168 20 25
169 Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly 45
170 35 40
171 Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile 60
172 50 55
173 Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly 80
174 65 70 75
175 Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro 95
176 85 90
177 Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn 110
178 100 105
179 Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser 120
180 115
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182 <211> LENGTH: 124
183 <212> TYPE: PRT
184 <213> ORGANISM: Mus musculus
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189 20 25
190 Pro Gly Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu 45
191 35 40
192 Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly 60
193 50 55
194 Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu

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195 65 70 75 80
196 Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg His Glu Val Tyr Ser Asp
197 85 90 95
198 Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile
199 100 105 110
200 Ser Gly Leu Met Pro Gly Ser Gly His Ser Arg Cys
201 115 120
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203 <211> LENGTH: 133
204 <212> TYPE: PRT
205 <213> ORGANISM: Mus musculus
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208 1 5 10 15
209 Ser Gly Ala Ser Trp Cys Leu Leu Phe Leu Pro Val Leu Leu Thr Val
210 20 25 30
211 Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe Pro Arg Cys
212 35 40 45
213 Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile Val Leu Gly
214 50 55 60
215 Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr Ser Leu Gly
216 65 70 75 80
217 Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr Arg Lys Gln
218 85 90 95
219 His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg
220 100 105 110
221 Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa
222 115 120 125
223 Ala Thr Leu Cys Pro
224 130
225 <210> SEQ ID NO 15
226 <211> LENGTH: 160
227 <212> TYPE: PRT
228 <213> ORGANISM: Mus musculus
229 <400> SEQUENCE: 15
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232 Gln Ser Asp Thr Phe Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly
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234 Val Leu Ala Gly Ile Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile
235 35 40 45
236 Ala Leu Ala Val Tyr Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly
237 50 55 60
238 Thr Ala Glu Gly Thr Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro
239 65 70 75 80
240 Tyr Gln Glu Leu Gln Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn
241 85 90 95
242 Thr Gln Arg Arg Tyr Tyr Arg Xaa Ala His Ser Met Pro Ile Ser Gly
243 100 105 110
243 Leu Met Pro Gly Ser Gly His Ser Arg Cys Leu Leu Asn Lys Pro Phe

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I403980.RAW

Line	? Error/Warning	Original Text
154	W "N" or "Xaa" used: Feature required	Gln Tyr Tyr Arg Xaa Ala His Ser Met Pro I
179	W "N" or "Xaa" used: Feature required	Thr Gln Arg Gln Tyr Tyr Arg Xaa Ala His S
198	W "N" or "Xaa" used: Feature required	Leu Asn Thr Gln Arg Gln Tyr Tyr Arg Xaa A
221	W "N" or "Xaa" used: Feature required	Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln A
242	W "N" or "Xaa" used: Feature required	Thr Gln Arg Arg Tyr Tyr Arg Xaa Ala His S
248	W "N" or "Xaa" used: Feature required	Xaa Asp Ile Xaa His Cys Thr Ile Ser Val P
282	W "N" or "Xaa" used: Feature required	Ser Asp Leu Asn Thr Gln Arg Gln Tyr Tyr A